



Form 1449 (Modified)		Any Docket No: MXGNP002X1	Application No.: 09/495,668
Information Disclosure Statement By Applicant (Use Several Sheets if Necessary)		Applicant: Selifonov et al.	
		Filing Date February 1, 2000	
		Group 1631	

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U.S. Patent Documents

TECH CENTER 1600/2900

Examiner Initial	No.	Patent No.	Date	Patentee	Class	Sub-class	Filing Date
	A1	6,125,331	9/26/00	Toh			
	A2	6,403,312	6/11/02	Bassil, et al			
	A3						

Foreign Patent or Published Foreign Patent Application

Examiner Initial	No.	Document No.	Publication Date	Country or Patent Office	Class	Sub-class	Translation	
							Yes	No
	B1	WO00/47612	8/17/00	WIPO				
	B2	WO01/61344	8/23/01	WIPO				
	B3	WO00/42559	7/2/00	WIPO				
	B4	WO01/75767	10/11/01	WIPO				

Other Documents

Examiner Initial	No.	Author, Title, Date, Place (e.g. Journal) of Publication
	C1	Young et al., "Characterization of Receptor Binding Determinants of Granulocyte Colony Stimulating Factor," <i>Protein Science</i> 6:1228-1236, 1997
	C2	Dahiyat and Mayo, "Protein Design Automation," <i>Protein Science</i> , 5:895-903, (1996)
	C3	Su et al., "Coupling Backbone Flexibility and Amino Acid Sequence Selection in Protein Design," <i>Protein Science</i> , 6:1701-1707, (1997)
	C4	Voigt et al., "Computationally Focusing the Directed Evolution of Proteins," <i>Journal of Cellular Biochemistry Supplement</i> , 37:58-63 (2001)
	C5	Hellberg et al., "Minimum Analogue Peptide Sets (MAPS) for quantitative Structure-Activity Relationships," <i>Int. J. Peptide Protein Res.</i> 37:414-427 (1991)



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<input checked="" type="checkbox"/>	C6	Martin van Heel, "A New Family of Powerful Multivariate Statistical Sequence Analysis Techniques," J. Mol. Biol, 220:877-887 (1991)
<input checked="" type="checkbox"/>	C7	Goldman et al., "Estimating Protein Function From Combinatorial Sequence Data Using Decision Algorithms and Neural Networks," Drug Dev. Research 33:125-132 (1994)
<input checked="" type="checkbox"/>	C8	Gustafsson et al., "Exploration of Sequence Space for Protein Engineering," J. Mol. Recognit. 14:308-314 (2001)
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<input checked="" type="checkbox"/>	C10	Chao Zhang, "Extracting Contact Energies From Protein Structures: A Study Using a Simplified Model," Proteins: Structure, Function, and Genetics, 31:299-308 (1998)
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<input checked="" type="checkbox"/>	C12	Miyazawa et al., "An Empirical Energy Potential With a References State for Protein Fold and Sequence Recognition," Proteins: Structure, Function, and Genetics, 36:357-369 (1999)
<input checked="" type="checkbox"/>	C13	Moore et al., "Predicting Crossover Generation in DNS Shuffling," PNAS, Vol. 98, No. 6, 3226-3231 (2001)
<input checked="" type="checkbox"/>	C14	Lehman et al., "Engineering Proteins for Thermostability: the Use of Sequence Alignments Versus Rational Design and Directed Evolution," Current Opinion in Biotechnology, 13:371-375 (2001)
<input checked="" type="checkbox"/>	C15	Colleen Kelly, "A Test of the Markovian Model of DNA Evolution," Biometrics 50, 653-664, (1994)
<input checked="" type="checkbox"/>	C16	H.W. Hellings, "Rational Protein Design: Combining Theory and Experiment," Proc. Natl. Acad. Sci. USA, Vol. 94, pp. 10015-10017, (1997)
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	C18	Jonsson, et al, "Quaintitative Sequence-Activity Modeils (QSAM)- Tool For Sequence Design", Nuclear Acid Research Vol. 21, No. 3, pp. 733-739 (1993)
	C19	Sjostrom, et al, "Signal Peptide Amino Acid Sequences In <i>Escheruchua coli</i> Contain Information Related To Final Protein Localization. A Multivariate Data Analysis", The CMBO Journal vol. 6, no. 3, pp 823-831, (1987)
	C20	Patel, et al, "Patenting Computer-Designed Peptides", Journal Of Computer-Acid Molecular Design 12 pp543-556, (1998)
	C21	Schneider, et al, "Peptide Design by Artificial Neural Networks and Computer-Based Evolutionary Search", Proc. Natl. Acad. Sci. USA, vol. 95, pp. 12179-121184, October 1998
	C22	Mee, et al, "Design of Active Analogues of a 15-Residue Peptide Using D-Optimal Design QSAR and a Combinatorial Search Algorithm", J Peptide Res. 49, pp. 89-102, (1997)
	C23	Bogarad, et al, "A Hierarchical Approach to Protein Molecular Evolution", Proc. Natl. Acad. Sci. USA, Vol. 96, pp. 2597-2595, March 1999
	C24	Darius, et al, "Simulated Molecular Evolution" Or Computer-Generated Artifacts?", Biophysical Journal, Vol. 67, pp. 2120-2122, November 1994
Examiner	Date Considered 2-4-05	

Examiner Initial citation considered. Draw line through citation if not in conformance and not considered. Include copy of this form with next communication to applicant.



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U.S. Patent Documents

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	B2							
	B3							
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	B5							

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	C2	Sheridan et al., "Using a Genetic Algorithm to Suggest Combinatorial Libraries," J. Chem. Inf. Compu. Sci., 35, 310-320, 1995
	C3	D.K. Agrafiotis, "Multiobjective Optimization of Combinatorial Libraries," IBM J. Res & Dev., Vol, 45, No. 3, 545-566, 2001
Examiner		Date Considered 2-4-05

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U.S. Patent Documents

Examiner Initial	No.	Patent No.	Date	Patentee	Class	Sub-class	Filing Date
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	A2	6,605,449 B1	08/12/03	Short	435	69.1	06/14/00

Other Documents

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	C2	SELIFONOV, Sergey A. et al., "Methods For Making Character Strings, Polynucleotides And Polypeptides Having Desired Characteristics", U.S. Patent Application No. 09/494,282, Filed 1/18/2000 (Our Dkt. MXGNP001X1)
	C3	SELIFONOV, Sergey A. et al., "Methods For Making Characteristics Strings, Polynucleotides And Polypeptides Having Desired Characteristics", U.S. Patent Application No. 09/539,486, Filed 3/30/200 (Our Dkt. MXGNP001X2)
	C4	SELIFONOV, Sergey A. et al., "Methods For Making Character Strings, Polynucleotides And Polypeptides Having Desired Characteristics", U.S. Patent Application No. 09/618,579, Filed 7/18/2000 (Our Dkt. MXGNP001X3)
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	C6	SELIFONOV, Sergey A. et al. "In Silico Cross-Over Site Selection", PCT Application No. PCT/US01/10231, Publication No. WO 01/75767 A3 (Our Dkt. MXGNP001X4WO)
Examiner	Date Considered 2-4-05	

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